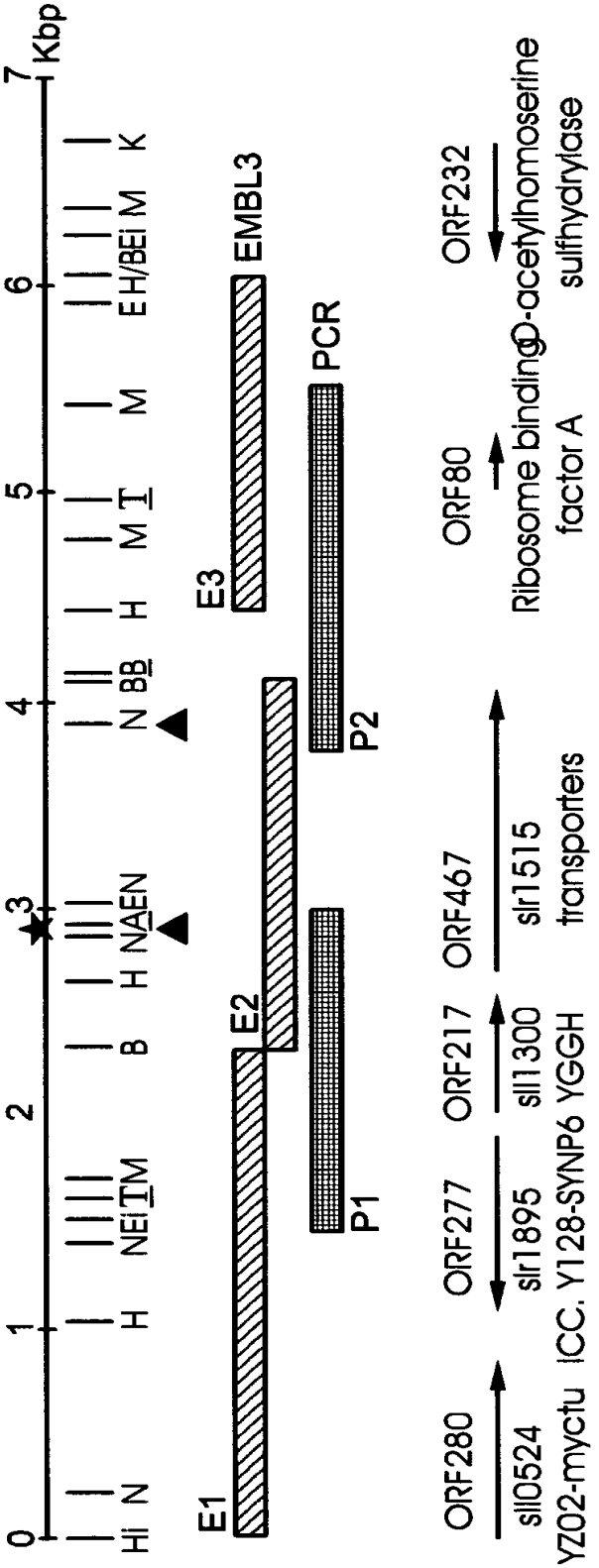

Fig. 1

```
ICTB : 1    ATGACTGTCTGGCAAACTCTGACTTTTGCCCATTACCAACCCCAACAGTGGGGCCACAGC 60 (SEQ ID NO:2)
SLR  : 13   ATCTCTATCTGGCGATCGCTGATGTTTGGCGGTTTTTCCCCCCAGGAATGGGGCCGGGGC 72 (SEQ ID NO:4)

ICTB : 61   AGTTTCTTGCATCGGCTGTTTGGCAGCCTGC-GAGCTTGGCGGGCCTCCAGCCAGCTGTT 119
SLR  : 73   AGTGTGCTCCATCGTTTGGTGGGCTGGGGACAGAG-TTGGATACAGGCTAGTGTGCTCTG 131

ICTB : 120  GGTTTGGTCTGAGGCACTGGGT--GGCTTCTTGCTTGCTGTCGTCTACGGTTCGGCTCCG 177
SLR  : 132  GCCCCACTTCGAGGCATTGGGTACGGCT-CTAG-TGGCAATAATTTTTATTGCGGCTCCC 189

ICTB : 178  TTTGTGCCCAGTTCCGCCCTAGGGTTGGGGCTAGCCGCGATCGCG-GCCTATTGGGCCCT 236
SLR  : 190  TTCACCTCCACCACCATGTTGGGCATTTTTAT-GCTGCTCTGTGGAGCCTTTTGGGCTCT 248

ICTB : 237  GCTCTCGCTGACAGATATCGATCTGCGGCAAGCA---ACCCCCATTCACTGGCTGGTGCT 293
SLR  : 249  GCTGACCTTTGCTGAT--CAACCAG-GGAAGGGTTTGACTCCCATCCATGTTTTAGTTTT 305

ICTB : 294  GCTCTACTGGGGCGTCGATGCCCTAGCAACGGGACTCTCACCCGTACGCGCTGCAGCTTT 353
SLR  : 306  TGCCTACTGGTGCATTTCGGCGATCGCCGTGGGATTTTCTCCGGTAAAAATGGCGGCGGC 365

ICTB : 354  AGTTGGGCTAGCCAAACTGAC-GCTC-TACCTGTTGGTTTTTGCCCTAGCGGCTCGGGTT 411
SLR  : 366  GTCGGGGTTAGCGAAATTAACAGCTAATTTATGTCTGTTTCTAC--TGGCGGCGAGGTTA 423

ICTB : 412  CTCCGCAATCCCCGTCTGC-GATCGCTGCTGTTCTCGGTCGTCGTGATCACATCGCTTTT 470
SLR  : 424  TTGCAAAACAAACAATGGTTGAAC-CGGTTAGTAACCGTTGTTTTACTGGTAGGGCTATT 482
```

Fig. 2a

Fig. 2a

Fig. 2b

Fig. 2c

Fig. 2

```
ICTB : 471  TGTCAGTGTCTACGGCCTCAACCAATGGATCTACGGCGTTGAAGAGCTGGCGACTTGGGT 530
SLR  : 483  GGTGGGGAGTTACGGTCTGCGACAACAGGTGGACGGGGTAGAACAGTTAGCCACTTGGAA 542

ICTB : 531  GGATCGCAACTCGGTTGCCGACTTCACCTCACGGGTTTACAGCTATCTGGGCAACCCCAA 590
SLR  : 543  TGACCCCACCTCTACCTTGGCCCAGGCCACTAGGGTATATAGCTTTTTAGGTAATCCCAA 602

ICTB : 591  CCTGCTGGCTGCTTATCTGGTGCCGACGACTGCCTTTT-CTGCAGCAGCGATCGGGGTGT 649
SLR  : 603  TCTCTTGGCGGCTTACCTGGTGCCCATGACGGGTTTGAGCTTGAGT-GCCCTGGTGGTAT 661

ICTB : 650  GGCGCGGCTGGCTCCCCAAGCTGCTGGCGATCG-CTGCGACAGGTGCGAGCAGCTTATGT 708
SLR  : 662  GGCGACGGTGGTGGCCCAAACTGCTGG-GAGCAACCATGGTGATTGTTAACCTACTCTGT 720

ICTB : 709  CTGATCCTCACCTACAGTCGCGGTGGCTGGCTGGGTTTTGTCGCCATGATTTTTGTCTGG 768
SLR  : 721  CTCTTTTTTACCCAGAGCCGGGGCGGTTGGCTAGCAGTGCTGGCCCTGGGAGCTACCTTC 780

ICTB : 769  GCGTTATTAGGGCTCTACTGGTTTCAACCCCGTCTACCCGCACCCTGGCGACGCTGGCTA 828
SLR  : 781  CTGGCCCTTTGTTACTTCTGGTGGTTACCCCAATTACCCAAATTTTGGCAACGGTGGTCT 840

ICTB : 829  TTCCCAGTCGTATTGGGTGGACTAGTCGCGGTGCTCTT-GGTGGCGGTGCTTGGACT--- 884
SLR  : 841  TTGCCCCTGGC----GATCGCC--GTGGCGGTTATATTAGGTGGGGGAGCGTTGATTGCG 894

ICTB : 885  -TG-AGCCGTTGCGCGTGCGCGTGTTGAGCATCTTTGTGGGGCGTGAAGACAGCAGCAAC 942
SLR  : 895  GTGGAACCGATTCGACTCAGGGCCATGAGCATTTTTGCTGGGCGGGAAGACAGCAGTAAT 954
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Fig. 2b

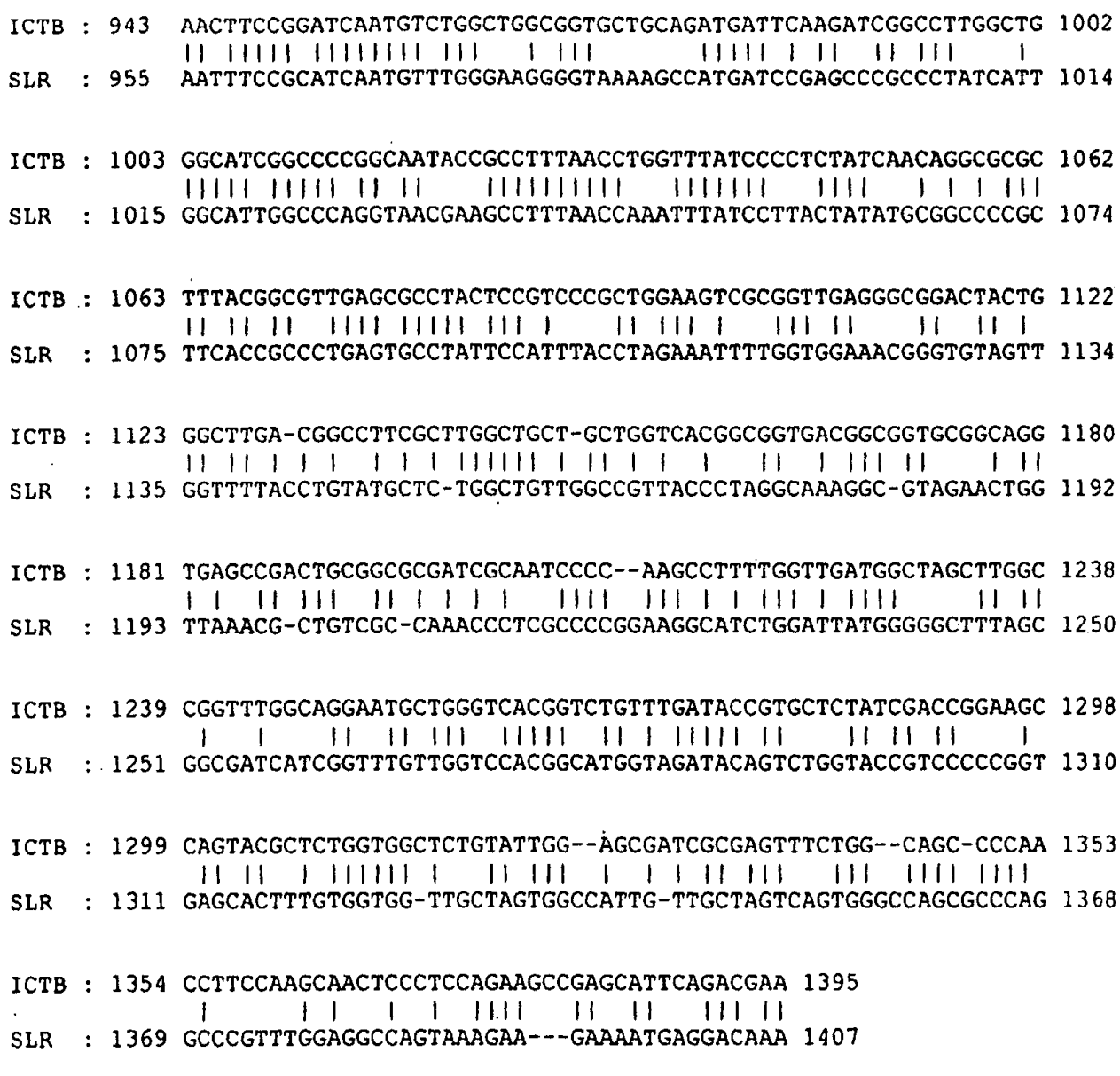

Fig. 2c

```
                +++W++L F  + PQ+WG  S LHRL G  ++W  +S L    EALG  L+A+++ +APF
SLR  : 5    ISIWRSLMFGGFSPQEWGRGSVLHRLVGWGQSWIQASVLWPHFEALGTALVAIIFIAAPF 64

ICTB : 61   VPSSALGLGLAAIAAYWALLSLTDIDLRQATPIHWLVLLYWGVDALATGLSPVRAAALVG 120
              ++ LG+ +    A+WALL+  D   +  TPIH LV  YW + A+A G SPV+ AA  G
SLR  : 65   TSTTMLGIFMLLCGAFWALLTFADQPGKGLTPIHVLVFAYWCISAIAVGFSPVKMAAASG 124

ICTB : 121  LAKLTLYLLVFALAARVLRNPRLRSLLFSVVVITSLFVSVYGLNQWIYGVEELATWVDRN 180
            LAKLT  L +F LAAR+L+N +  + L +VV++  L V  YGL Q + GVE+LATW D
SLR  : 125  LAKLTANLCLFLLAARLLQNKQWLNRLVTVVLLVGLLVGSYGLRQQVDGVEQLATWNDPT 184

ICTB : 181  SVADFTSRVYSYLGNPNLLAAYLVPTTAFSAAAIGVWRGWLPKLLAIAATGASSLCLILT 240
            S     +RVYS+LGNPNLLAAYLVP T  S +A+ VWR W PKLL       + LCL  T
SLR  : 185  STLAQATRVYSFLGNPNLLAAYLVPMTGLSLSALVVWRRWWPKLLGATMVIVNLLCLFFT 244

ICTB : 241  YSRGGWLGFVAMIFVWALLGLYWFQPRLPAPWRRWLFPVVLGGLVAVLLVAVLGLEPLRV 300
             SRGGWL  +A+   + L  +W+ P+LP  W+RW  P+ +   V +   A++ +EP+R+
SLR  : 245  QSRGGWLAVLALGATFLALCYFWWLPQLPKFWQRWSLPLAIAVAVILGGGALIAVEPIRL 304

ICTB : 301  RVLSIFVGREDSSNNFRINVWLAVLQMIQDRPWLGIGPGNTAFNLVYPLYQQARFTALSA 360
            R +SIF GREDSSNNFRINVW  V  MI+ RP +GIGPGN AFN +YP Y + RFTALSA
SLR  : 305  RAMSIFAGREDSSNNFRINVWEGVKAMIRARPIIGIGPGNEAFNQIYPYYMRPRFTALSA 364

ICTB : 361  YSVPLEVAVEGGLLGLTAFAWLLLVTAVTAVRQVSRLRRDRNPQAFWLMASLAGLAGMLG 420
            YS+ LE+ VE G++G T   WLL VT    V  V R R+   P+  W+M +LA + G+L
SLR  : 365  YSIYLEILVETGVVGFTCMLWLLAVTLGKGVELVKRCRQTLAPEGIWIMGALAAIIGLLV 424

ICTB : 421  HGLFDTVLYRPEASTLWWLCIGAIASFWQPQPSKQLPPEAEHSDEKM 467
            HG+ DTV YRP  STLWWL +  +AS W    ++    + E+ D+ +
SLR  : 425  HGMVDTVWYRPPVSTLWWLLVAIVASQWASAQARLEASKEENEDKPL 471
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Fig. 3

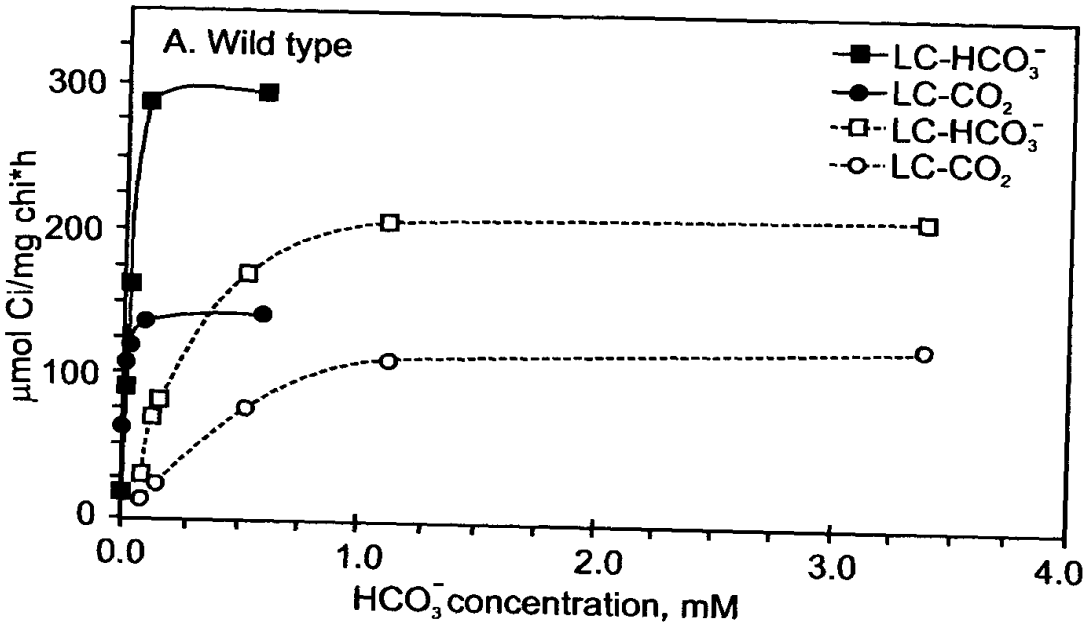

Fig. 4a

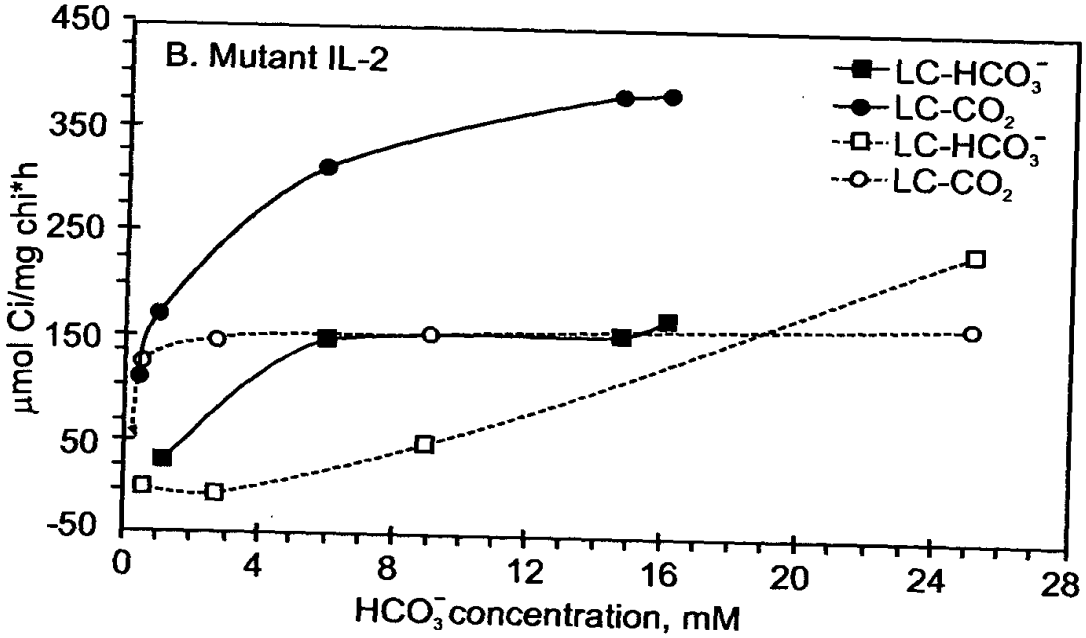

Fig. 4b

Wild type	GGGCT-AGCCGCGATCGCGGCCTATTGGGCCC	(SEQ ID NO:6)
IL-2 *Apa*I side	GGGCT-AG--G-GATCGC-GCCTATTGGGCCC	(SEQ ID NO:7)
IL-2 *Bam*HI side	GGGCTCA-----GATCGC-GCCTATTGGGCCC	(SEQ ID NO:8)
IctB	G L A A I A A Y W A L	(SEQ ID NO:9)

Fig. 5

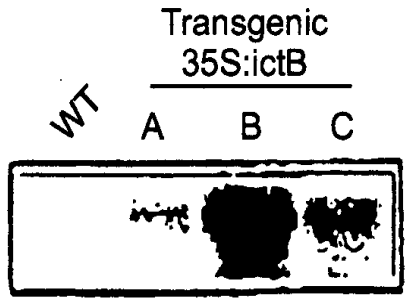

Fig. 6